

RT	"Molecular characterization of the major maize embryo globulin encoded by the Glb1 gene."
RT	Plant Physiol. 91:636-643(1989).
RN	(2)
RP	SEQUENCE OF 87-100.
RX	MEDLINE=89374022; PubMed=2775172;
RA	Kriz A.L.:
RT	"Characterization of embryo globulins encoded by the maize Glb genes."
RL	Biochem. Genet. 27:239-251(1989).
CC	-1- PWM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE MAJURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
CC	-1- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL PROTEINS, RESPECTIVELY.
CC	-1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
CC	-----
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CC	-----
DR	EMBL; M24845; AAA33467.1; "
DR	HSSP; P50477; ICAM.
DR	MAI2EDB; 30181; "
DR	INTERPRO: IPR001113; "
DK	PfAM; PF00546; Seedstore_7s; 1.
MW	Seed storage protein; Signal.
FT	SIGNAL 1 18 OR 21 (POTENTIAL).
FT	PROPEP 19 86
FT	CHAIN 87 573 GLOBULIN-1 S ALLELE.
FT	CARBOHD 349 349 N-LINKED (GLUCAC...) (POTENTIAL).
SO	SEQUENCE 573 AA; 65029 MW; 525EDID00A052976 CRC64;
<hr/>	
Query Match	25.6%; Score 905; DB 1; Length 573;
Best Local Similarity	39.9%; Pred. No. 1,1e-48;
Matches 201; Conservative 91; Mismatches 180; Indels 32; Gaps 10;	
OY	182 EDNRKRDPOQRVEDRCRRCEQERPDQHOCQLRCREDOGRHGRGDMN-PORGSG-- 238
Db	25 EDDNNHHHGKSGRCVRCEDRPMHQRPCLDCCREREERKRQERSRHENADRRSGEGSS 84
OY	239 -----RYEEGEESQSD-NPYFDEDSLSTRRTTEGHISYLENFPGRSKLRLALKNYRLV 292
Db	85 EDEREERKEKEKKQDRPVYVFDRSFRRVVVSSEGSIIRYLRFDEYSRLRGIRDYVVA 144
OY	293 LLEAPNAFVEPTIHDAALILLVIGSRALKMIHNINDNESYNLEGDVIRIPAGTFPLI 352
Db	145 VLEANRSEFVVPSSHDAICIGVAEGEVATTIENGERSTTIQGNHFVARPAQAVITLA 204
OY	353 NRDNNEHLIAFLQTISTPGQYKEFFPAGQONPREVLSTFSKETLEALNTQTEKLGCV 412
Db	205 NTDGKKKVIKTHLTITSVPEFOFFFGGRPNDESFLSPSKSIQRAKYXTSSDLREL 264
OY	413 FGO--QRGCIYIARSODRIELTRDDSE---SRMHILFRGESSRGCPNLFNKRPLYSNK 467
Db	265 FGRRGQODGIIVATERDETRELRRHASCGCHPWLPDPPE-SRGPYSLIDORPSIANQ 323
OY	468 YGQAEVYEPREDYRLOLDMDLSVFATYVOCGMOPFEFTSTKVUVVASGADVEMACP 527
Db	324 HCOLYEANARBFHDLAENDVSVSFANTTAGMSAPRLYNTBSFKLIAYVPNGCYAEIYCPH 383
OY	528 LSGRHG----GRGGCKRHEEEDVHYDQ-----VRALSKREALIVLVLAGHPVYVS 574
Db	384 ROSQGEGESEBERGKGRRSEEESESSEDEVGQGYHTIRALTSGTAFVYPAGRPYAVA 443
OY	575 SGNERLLLFAGCINAQNHNENFLAGRERNVLOETIPQAMELATAPRKVEEESFNSDQS 634

Db	444	SRDSNU4TVCPEVHADNRNEKVEYLACAD-NVLQKIDRVAKALSFASKAEVDEVLSRREK	502
Qy	635	IFPQPRP---HQOQSPRSTKQOQ	655
		:: :: ::	
Db	503	GFLPGPKESGGHEEREDEEREERE	526
RESULT 4			
ID	GLCX_SOYBN	STANDARD:	PRT; 639 AA.
AC	P11827;		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	01-AUG-1992 (Rel. 23, Last annotation update)		
DE	BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR.		
GN	Cg-1.		
OS	Glycine max (Soybean).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC	Fabales; Fabaceae; Papilionoideae; Glycine.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86250867; PubMed=3013879;		
RT	Doyle J.J., Schuler M.A., Godelle W.D., Zenger V., Beachy R.N.,		
RT	Slightom J.L.;		
RT	"The glycosylated seed storage proteins of Glycine max and Phaseolus		
RT	vulgaris. Structural homologs of genes and proteins."		
RL	J. Biol. Chem. 261:9228-9238(1986).		
RN	[2]		
RP	SEQUENCE OF 340-639 FROM N.A.		
RX	MEDLINE=83143289; PubMed=6897678;		
RA	Schuler M.A., Ladin B.F., Pollaco J.C., Freyer G., Beachy R.N.;		
RT	"Structural sequences are conserved in the genes coding for the		
RT	alpha, alpha' and beta-subunits of the soybean 7S seed storage		
RT	protein."		
RL	Nucleic Acids Res. 10:8245-8261(1982).		
CC	-1- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED		
CC	DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A		
CC	CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.		
CC	-1- SUBUNIT: THE ALPHA', ALPHA' AND BETA-SUBUNTS ASSOCIATE IN		
CC	VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.		
CC	-1- SUBCELLULAR LOCATION: CYTOLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN		
CC	BODIES.		
CC	-1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,		
CC	CONVULCIN, CONGLYCININ, ETC.).		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@lsb-sib.ch).		
CC	-----		
DR	EMBL: M13759; AAB01374.1; -		
DR	EMBL: J01290; -; NOT_ANNOTATED.CDS.		
DR	PIR: B24810; B24810.		
DR	HSSP: P02853; 2PHT.		
DR	INTERPRO: IPR001113; -		
DR	PFAM: PF00546; Seedstore_7s; 2.		
KW	Seed storage protein; Signal; Glycoprotein; Multigene family.		
FT	SIGNAL	1 22	
FT	PROPEP	23 62	
FT	CHAIN	63 639	BETA-CONGLYCININ, ALPHA' CHAIN.
FT	CARBOHYD	277 277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	551 551	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	543 543	P -> L (IN REF. 2).
FT	CONFLICT	549 549	M -> V (IN REF. 2).
FT	CONFLICT	608 608	S -> T (IN REF. 2).
SO	SEQUENCE	639 AA; 74325 MW; 469BFB24C79651E3F CRC64;	


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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ALLERGEN ARA H I, CLONE P17 (ARA H I).
OS Atachis hypogaeae (Peanut).
OC Magnoliophyta: Viridiplantae; Embryophyta: Tracheophyta; Spermatophyta;
OC Eukaryota; eudicotyledons: core eudicots: Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Arachis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FLORUNNER;
RX MEDLINE=96013631; PubMed=7560062;
RA Burks A.W., Cockrell G., Stanley J.S., Helm R.M., Bannon G.A.;
RT "Recombinant peanut allergen Ara h I expression and IgE binding in
RT patients with peanut hypersensitivity.";
RL J. Clin. Invest. 96:1715-1721(1995).
CC -1- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL; L38853; AAA60336.1; -.
DR HSSP; P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
KW Allergen.
SQ SEQUENCE 614 AA; 70283 MW; 1DDACF217EECF31 CRC64;

Query Match          24.0%; Score 849; DB 1; Length 614;
Best Local Similarity 34.7%; Pred. No. 3.3e-45;
Matches 219; Conservative 110; Mismatches 216; Indels 86; Gaps 21;

QY 70 SKYDNEPOTEC-QQCORCRQDQSGPRQOQYQCRCKEICEEEREYERQRPQOQEQ 128
DB 27 SPYKTEBNP---CAORCLQSC-QQEPDLKQKCESRCTL-----EY-----DPRCYD- 72
QY 129 CQKHQCRREPRIMQTCQORCERREYERKQOQKREDOQREDEEYERMEEDNRD 188
DB 73 -----TGANORHPRGERKRGPRGPDYDDRRQPRREEGRGMPAPRPREDEED-WRQ 125
QY 189 PQOEYEDCRRRCQDQRPQOQOQLRCRQOHRGGMNPRQSGSRYEGEREQS 248
DB 126 PR-----EDMRPSHQO-PR-----KIRREGGE-----QEWGTGSEVERETS 165
QY 249 DNPYFEDERSLSTRFTEEGHISVLENFYGRSKLLRALKMYRLVLEFANPAEVLPT 308
DB 166 NNPFFPSRFRSTRYGQNGRIRVLRQRFDRSKQFQNLQHRITVQTLARNTLVLP 225
QY 309 ADAILVYGRGALKMHHNRESYNLECGDVIRIPAGTFFYLINDNRLHIATKLOT 368
DB 226 ADNLIVYQQAQAVTVANGNRKSFNDEGHARIPSGFTSYLIRHDNONLHVAKISMP 285
QY 369 ISTPGQYKEFFPAGQNPPELYLSPFSKEILEALNTOETKLRGVF-----GQQ 416
DB 286 VNPFGQFEDFFPSSRQSSYLQGFSSNTLEAFNMAEFNIRVLLLEENAGDOBERGQR 345
QY 417 R-----EGVIRASQEOIRELTRDSDSRHMIIRGGS--RGPNYLFNKRPYLSN 466
DB 346 RRSRSSDNGSVLVKYSKEHVQELTKHAKSVS-----KQSEEDITNPILNRGPE 401
QY 467 KYQQAIVKREEDR-QLODMDSLVTANTQSGMAGPFFETASTKYVVAAGADVEMAC 525
DB 402 NFRLEVEYKDKKNPOLQDDMLTCEVIEGALMLPHFNKAMVIVVAKGTGNELVA 461
QY 526 PHLSGRGGGGGRHREEDVAHYE---QVR---ARLSREALIVLAGHPVVFVSSGNE 578
DB 462 VRKEDQQRGRREDEEEDDEEBSNREVRITRLKGDVFIIPAHPAIVAINSSSEL 521

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QY 579 NLLFAFGINQNNHNFELAGREHNVLOQIEPQAMELAFAPRKEVEESFNQDSIFFP 638
DB 522 HLL--GFGINAEHNRHLEFGDKRONVIDQIEKQAKDLAPGSGQGVKLLKNQREH 579
QY 639 G-PRHQOQSPRSTKQOQ-----PLVSTL 661
DB 580 ARPQOSQSPSSPEKEDQEEENQGGKGPILSTL 610

RESULT 7
ID GLCA_SOYBN STANDARD; PRT; 605 AA.
AC P13916;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BETA-CONGLYCININ, ALPHA CHAIN PRECURSOR.
OS Glycine max (Soybean).
OC Magnoliophyta: Viridiplantae; Embryophyta: Tracheophyta; Spermatophyta;
OC Eukaryota; eudicotyledons: core eudicots: Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COTYLEDON;
RX MEDLINE=91355860; PubMed=2103438;
RA Sebastiani F.L., Farrell L.B., Schuler M.A., Beachy R.N.;
RT "Complete sequence of a cDNA of alpha subunit of soybean beta-
RT conglycinin.";
RL Plant Mol. Biol. 15:197-201(1990).
CC -1- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED
CC DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A
CC CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
CC -1- SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE IN
CC VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
CC -1- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRANE-BOUND
CC VACUOLAR PROTEIN BODIES.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
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CC -----
CC EMBL; X17698; CAA35691.1; -.
DR PIR; S14681; FWSYBA.
DR HSSP; P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal; Glycoprotein; Multigene family.
FT SIGNAL 1
FT PROPEP 23
FT CHAIN 63
FT CARBOHYD 261
FT CARBOHYD 517
SQ SEQUENCE 605 AA; 70293 MW; CBEBA30506BBBC57 CRC64;

Query Match          23.7%; Score 840.5; DB 1; Length 605;
Best Local Similarity 30.5%; Pred. No. 1.1e-44;
Matches 205; Conservative 144; Mismatches 223; Indels 101; Gaps 17;

QY 11 LFLFLSLFLSTTVS--LAESEFDRQYECKRQCMQLETSGQMRQVSGQCRKRFEDID 68
DB 8 LLLGLGVFLASVSVSGIAYWEKENPKHNKCLQCSERDSRYNQACHARC-----N 59
QY 69 WSKYDNEPQTPQCCQCRCRQDQSGPRQOQYQCRCKEICEEEREYERQRPQOQEQ 125
DB 60 LTKVERKECEGEIIPRPRQHPREPRQOQGE-----KEEDEDPRIPIPRPQO 110

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DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
GN SBP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
RC TISSUE-EMBRYO:
RX MEDLINE=93104680; PubMed=1467654;
RA Grimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D.;
RT "A 62-kD sucrose binding protein is expressed and localized in
RT tissues actively engaged in sucrose transport.";
RL Plant Cell 4:1561-1574(1992).
CC -1- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC -1- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
CC SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
CC MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
CC MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
CC -1- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
CC UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
CC FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
CC DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
CC EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
CC RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06038; AAB03894.1; -.
DR PIR; J01730; J01730.
DR HSSP; P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PRAM: PR000546; Seedstore_7s; 1.
KW TRANSPORT; Sugar transport; Signal; Membrane.
FT SIGNAL 1 29
FT CHAIN 30 524 SUCROSE-BINDING PROTEIN.
SQ SPROUNCE 524 AA; 60522 MW; 0251EB90796EF341 CRC64;

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Query Match 22.8%; Score 808; DB 1; Length 524;
Best Local Similarity 33.9%; Pred. No. 9,1e-43;
Matches 194; Conservative 97; Mismatches 179; Indels 102; Gaps 17;

QY 105 KCEYECEEYKRRPRPQ--QQYECCOKHCORREPRMOTCCQRCERREYKERRKQ 162
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
27 KCEYECEEYKRRPRPQ--DPELVCKHCQOQOQYTESGKR--VCLQSCD-RYHMKQERE 76
CC -----
QY 163 KRYEEDERDEKYEERKEDNKRPOQREYEDCRRRCQEQPRROHCOLRCREQORQ 222
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
77 KQIQEYERKEKEE-ESERE-----EQEQ 101
CC -----
QY 223 HGRGDMANFQRGSGRYEGEEDSDNRYFDE-NSLSTRFTEEGHSLVENYGRSK 291
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
102 H-----EEDENPFIPEEDKDFETRYETEGGRILRYLKKFTFKSK 140
CC -----
QY 282 LRLAKNRYLVLEANDPNAFVLPTHLDADAILLVIGRGALKMHHNDNSYLVLEGDVI 341
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
141 LQGIETFRALIEARAHFTVSFRHFDSEVFNIGRAVLGVASSETEKTLLEGDMT 200
CC -----
QY 342 RIPAGTFEVLINDDNRLHIA--KFLQITSPGQYKEFPAGQONPEPYLSTFSKEILE 399
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 HIRAGPPLVIVNDENDKILFLAMLHLPVSYSTGKFEFFAPGRPEVSLAFSNVNIQ 260
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 AALNTOTEKRGVGGQOREGVITIRASQOIRLTDSDSRIHWHIRRGSSRGPNLEN 459
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 261 AALQTPKGLKNVFDQDNEGSIFRISREQVRLA-PTKSSMWP--GGE-SKQFNIFS 316
QY 460 KRLPYSNKYGQAEVREKEDRO--LQMDLSVFIANTQCSMMGPFNTSTVYVAVASG 517
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
317 KRLPYSNKYGQAEVREKEDRO--LQMDLSVFIANTQCSMMGPFNTSTVYVAVASG 517
QY 518 EADVEMACPHLSGRHGSGGGRKHEEEDVHYEQVRLSKREAIIVLAGHPVVFVSSGN 577
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
377 RGHQIQSCIPHMS-----SRSSSHKDKSSP--SYHRISDLKPGWVFVPPCHPTVATSNK 431
QY 578 ENLLIFAFGINAQNHNENFLAGRENVLQOIEPQAMELAFAPKEVEESF----- 628
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
432 ENLLIFAFGINAQNHNENFLAGRENVLQOIEPQAMELAFAPKEVEESF----- 628
QY 629 -----NSQDSIFFPQPGHQOQSPRS 650
DB :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
491 LIGRLYHLPHKRESEFFPELPRERGRRA 522

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RESULT 10
VCIL_PEA STANDARD; PRT; 459 AA.
ID VCIL_PEA
AC P13918;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VICILIN PRECURSOR.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEEDLING;
RA Higgins T.D.V., Newbigin E.J., Spencer D., Llewellyn D.J., Craig S.;
RT "The sequence of a pea vicilin gene and its expression in transgenic
RT tobacco.";
RL Plant Mol. Biol. 11:683-695(1988).
RN [2]
RP SEQUENCE OF 27-459 FROM N.A. (CLONE P00B9).
RC STRAIN=CV. FELTHAM FIRST;
RX MEDLINE=88326226; PubMed=3046604;
RA Watson M.D., Lambert N., Delauney A., Yarwood J.N., Croy R.R.D.,
RA Gatehouse J.A., Wright D.J., Boulter D.;
RT "Isolation and expression of a pea vicilin cDNA in the yeast
RT Saccharomyces cerevisiae.";
RL Biochem. J. 251:857-864(1988).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
CC BODIES.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 11 GENES FOR VICILIN SUBUNTS,
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
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CC -----
DR EMBL; X14076; CAA32239.1; -.
DR EMBL; Y00722; CAA68708.1; -.
DR PIR; S00567; S00567.
DR PIR; S08505; S08505.
DR HSSP; P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PRAM: PR000546; Seedstore_7s; 1.
KW Seed storage protein; Multigene family; Signal.
FT SIGNAL 1 28
FT CHAIN 29 459 VICILIN.

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RX	MEDLINE=83220791; PubMed=6667941;	
RA	LYCETT G.W., Delaney A.J., Gatehouse J.A., Gilroy J., Croy R.R.D.,	
RA	Boulter D.;	
RT	"The vicillin gene family of pea (<i>Pisum sativum</i> L.): a complete cDNA	
RT	coding sequence for preprovicillin."	
RL	Nucleic Acids Res. 11:2367-2380(1983).	
CC	-1- FUNCTION: SEED STORAGE PROTEIN.	
CC	-1- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN	
CC	BODIES.	
CC	-1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,	
CC	CONVICILIN, CONGLYCININ, ETC.).	
DR	PIR: A03344; EMPMB.	
DR	HSSP: P50477; ICAM.	
DR	INTERPRO: IPR001113; -.	
DR	PRAM: PF00546; Seedstore_7s. 1.	
KW	Seed storage protein; Glycoprotein; Multigene family; Signal.	
FT	SIGNAL.	1
FT	CHAIN	16
FT	STATE	221
FT	CARBOHYD	359
FT	NON_TER	410
FT	SEQUENCE	410 AA; 46385 MW; 8AF68CE85A316FA2 CRC64;

Query March	19.7%	Score 699.5;	DB 1,	Length 410;
Best Local Similarity	36.9%	Pred. No. 3.1e-36;		
Matches 147; Conservative	79;	Mismatches 143;	Indels 29;	Gaps 5,

QY	249	DNVYEDERLSIPFRTPEEGHISYLEMFGYRSKTLRALKNVRLVLEANPAVLPPTH	308
Db	20	ENPTEFSNRPÖTYLENENGHIRLQFOFKRSJFENLOWRILLEYKSKETHLPDYTD	79
QY	309	ADAILVIGGRGALKMHNHDRESYNECCGDVIRIPAGTFYILIRNNRRLHIAKFLQ	368
Db	80	ADFLVILSKATLVTYLAKSNDRNSFNEBRDAILKPLAGSIAFYANRDRDNEPRVLDLAI	139
QY	369	ISTPQYKFEFFPAGGONPEPLTFSFEKILDEALNLTOTEKLRGVFGOR-----	417
Db	140	VNKRQLOSLFLSTGTONOKSLSGFSKNILLEAFNTYVELEKVLLEQOEOPHRSLK	199
QY	418	-----EEVITRASOEOLRELTRODSERHMIIRCGSSSGRYLFLFKRPLYSKYG	465
Db	200	DRROEINEENVYIAKVSXDOJELSKNKKSS---KXSVSESGPEMLRSRNPYISKFG	255
QY	470	QAVEVPEPDYROLQDMDSLFYIANVTGSGMKGPEFNTSRFVVVYVAGSDVEMACPILS	529
Db	256	KFEFLTEPKNQLODDLDIFVNSVDIKKGSLLRPYNSRALIVITVTGKODFELYGR--	313
QY	530	GRHGCGGGGRHHEEDV--HYEOWRRLSKREALIVLAGHPVYVSSGNETLLFAFGI	587
Db	314	NENQCKENDEEEOEETSKOYOLYRAKLSPGDVFVIRPACHPAVALNASSDLNLI--GLGI	371
QY	588	NAONNHENFLAGRANVLOQIFQAMDLAARPKVE	625
Db	372	NAENNERNPLAGEEDVIAISOVERPKVLAPGSSHEVD	409

RESULT	13
VCL_VICFA	
ID	STANDARD; PRT; 463 AA.
AC	P08438;
DT	01-AUG-1988 (Rel. 08, Created)
DT	01-AUG-1988 (Rel. 08, Last sequence update)
DT	01-JAN-1990 (Rel. 13, Last annotation update)
DE	VICILIN PRECURSOR.
OS	Vicia faba (Broad bean) .
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta
OC	Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosids I;
OC	Fabales: Fabaceae: Papilionoideae: Vicia.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-CY. MINOR;
RC	MEDLINE=88096511; PubMed=3697075;
XX	

RA Meschke W., Baumannlein H., Mobus U.:
RT "Nucleotide sequence of a field bean (*Vicia faba* L. var. minor) vicilin
RT gene.";
RL Nucleic Acids Res. 15:10065-10065(1987).

RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. FRIBO:
RX	MEDLINE=88067789; PubMed=3684610:
RA	Bassuener R., van Nong H., Jung R., Saalbach G., Muentz K.,
RT	"The primary structure of the predominating vicillin storage protein
RL	subunit from field bean seeds (<i>Vicia faba</i> L., var. minor cv. Fribor).";
CC	Nucleic Acids Res. 15:9609-9609(1987).
CC	-1- FUNCTION: SEED STORAGE PROTEIN.
CC	-1- SUBCELLULAR LOCATION: CYTOSOL; VACUOLAR MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.
CC	-1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
CC	

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DR	EMBL; Y00506; CA68559.1; -.	
DR	EMBL; Y00462; CA68525.1; -.	
DR	PIR; S06309; S06309.	
DR	PIR; A27288; A27288.	
DR	HSSP; P50477; ICAM.	
DR	INTERPRO; IPR00113; -.	
DR	PRAM; PF00546; Seedstore_7s; 1.	
KW	Seed storage protein; Signal.	
FT	SIGNAL	1
FT	CHAIN	28
FT	CONFLICT	257
FT	CONFLICT	443
FT	CONFLICT	443
Q	SEQUENCE	463 AA; 52694 MW; 5CD09FEFD0D5E685 CRC64;

Query Match	19.7%	Score 697.5	DB 1	Length 463
Best Local Similarity	35.1%	Pred. NO. 4.0e-36		
Matches 154; Conservative	89;	Mismatches 159;	Indels 37;	Gaps 6;

QY	249	DNPVYEDERLSURFRNREESHSVLEMEFGYRSKTLRYKRLVYLLEAMNAPVLPYRHL	3008
Db	33	DNPVFEESNRFOJTEFENENSHIRLQAFDOHSKILLENQVRLLEKYSKPHITFLPQD	92
QY	309	ADAILVIGGRGALKMTHHNRESYVNECCGDVIRIPAGTFYILINPNRNERLIHAKPIOT	3668
Db	93	ADFLVVLVLSKALITVLLPRDRMSFLEBRDITIKLPAGTIGLYVNRDDEDLAVLDLVP	1522
QY	369	ISTPQYKEFFPAGGONPEPYLSTFSKELLEALNPTQELKGVFO-----	4155
Db	153	VNRPGEPOSFLSGNQNOPSILSGFSKNILEASFNTDYKEIEKVLLEHGEKHYHRGLK	2122
QY	416	-----ORECVIIRASDQIRRELTRODSBERHMHIRRGSGSSGPNYLFNKKRLYSKYG	4659
Db	213	DRROGEEENVYIKISKROIEELNKKASS---KSTSESEFPNLRREPLYSKPG	268
QY	470	QAVEYKPEDRLOLQMDLVSFIANVTGSMAGPEFNTRSFYVVAAGSDVEMACPHLS	5299
Db	269	KFEFLTPKRNPRLODLNLFVNYVEINGSTLLRHYNSRALIVTVANGKDFPELVQRNE	3288
QY	530	GRHGGGGRGGRHEEDDVHYEYR-----ARLSKREALIVLAGRPVYFVSSGNEMLL	5823
Db	329	NOOGLR---EYDEEEKGEGEETIRKQYQNKAKLSPDVLVIPAGVPVAIKASSNLTV-	3804
QY	583	FAGCINANNHFNFLAGRENNVLOQIEPQAMELAFAPARKVEVEESFNSOOSITFFPGPRQ	6422
Db	385	-GGVIANENNQRYFLAGEEDNVISQIHKPKVKELPASQAEVDVTLLENOKOSHANAPR	4433

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QY 643 HQOQSPRSTKQOQPLVSIL 661
DB 444 EREGRSOEIKDH--LYSIL 460

RESULT 14
CANAVA_CANGN STANDARD; PRT; 445 AA.
ID CANA_CANGN
AC P50477;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
OS CANAVALIN PRECURSOR.
OC Canavalia ensiformis (Jack bean) (Horse bean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Canavalia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COTYLEDON;
RX MEDLINE=92119225; PubMed=1731967;
RA Ng J.D., Stinchcombe T., Ko T.-P., McPherson A.;
RT "PCR cloning of the full-length cDNA for the seed protein canavalin
RT from the jack bean plant, Canavalia ensiformis.";
RL Plant Mol. Biol. 18:147-149(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=COTYLEDON;
RX MEDLINE=94143475; PubMed=8310055;
RA Ng J.D., Ko T.-P., McPherson A.;
RT "Cloning, expression, and crystallization of jack bean (Canavalia
RT ensiformis) canavalin.";
RL Plant Physiol. 101:713-728(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=94143476; PubMed=8310056;
RA Ko T.-P., Ng J.D., McPherson A.;
RT "The three-dimensional structure of canavalin from jack bean
RT (Canavalia ensiformis)."
RL Plant Physiol. 101:729-744(1993).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
CC -----
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CC -----
DR EMBL: X59467; CAA42075.1; -
DR PDB: 1CAU; 31-OCT-93.
DR PDB: 1CAV; 31-OCT-93.
DR PDB: 1CAW; 31-OCT-93.
DR PDB: 1CAX; 31-OCT-93.
DR INTERPRO: IPR001113; -
DR PFAM: PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 27 445 BY SIMILARITY.
FT CHAIN 1 26 CANAVALIN.
SQ SEQUENCE 445 AA; 50326 MW; 30383C5F83A1E9B7 CRC64;

Query Match 19.0%; Score 674; DB 1; Length 445;
Best Local Similarity 33.3%; Pred. No. 1.3e-34;
Matches 143; Conservative 101; Mismatches 159; Indels 26; Gaps 6;

QY 235 GSGRGEEDS---DNPYFDESLSTRFTEGHSVLENFYGRSKLLRALKNYRL 291
DB 29 GHSGEAEDESESRANNNPYLFRRSNKKFLTLFKNQHGSLRLQRFNEDYEKLENLADRYR 88

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QY 292 VILEANPNAEVLEPTHLADAILLVIGRGALKMIIHNDRESYNLECGDYIRIPAGTFFYL 351
DB 89 LEYCSKPNFTLLPHHSDDSLDLVLEGOAILLVNPDGRDPTXLDGDAIKIOAGTFPL 148

QY 352 INRDNNERHLIAKFLQTIISPGQYKEFPFAGGONPEPPIYSTPSKELLEALNTQTKL-R 410
DB 149 INPDNNONNLILKFAITFRPPGTVEDEFFLSSTKRLPSYLSAFKNFLASYSYPDEIQ 208

QY 411 GVFGQOREGVIIRASOQIRELFRDDESESRHMIIRGGESSRPYULFNKRPILSKYGO 470
DB 209 TLIOEEOEGYIVAMPKDQIOETSKHAOSS----KRTLSQDKPFYURSDPITYSNNYCK 264

QY 471 AYEVRKEDYRQLODMQLSVFIANVTGSMGWPEFNTSTKRVVAVSGEADVEMACPILSG 530
DB 265 LYEITPEKNSQRLDLDILLNCLQMEGALFVPHNSRATVILVANGRAVELV----- 318

QY 531 RHGGRGGKRHEEEDVHYEQVR---ARLSKRALIVYLACHPVVFPVSSGNNILLFAFGI 587
DB 319 -----GLEOQOQGLIESMQLRRYATLSEGDIIIVIPSSFYALKAASDLNMY--GIGV 369

QY 588 MAQNNHENFLAGRRVNLQOIEPQAMELFAAPRKVESEFSNSQDSIFPPGPROHQQS 647
DB 370 MAENNERNFLAGKENVRIQIPROVSDLTTPGSGEVEELLENMOKESFYVDGPPRIDAG 429

QY 648 PRSTKQOOP 656
DB 430 GKARRAHLR 438

RESULT 15
CANAVA_CANGL STANDARD; PRT; 445 AA.
ID CANA_CANGL
AC P10562;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CANAVALIN PRECURSOR.
OS Canavalia gladiata (Sword bean) (Japanese jack bean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Canavalia.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-40.
RC TISSUE=SEED;
RX MEDLINE=88111636; PubMed=3338449;
RA Yamauchi D., Nakamura K., Asahi T., Minamikawa T.;
RT "cDNAs for canavalin and concanavalin A from Canavalia gladiata
RT seeds. Nucleotide sequence of cDNA for canavalin and RNA blot
RT analysis of canavalin and concanavalin A mRNAs in developing seeds.";
RL Eur. J. Biochem. 170:515-520(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RX MEDLINE=89296493; PubMed=2740227;
RA Takei Y., Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of the canavalin gene from Canavalia gladiata
RT seeds.";
RL Nucleic Acids Res. 17:4381-4381(1989).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CC CONVICILIN, CONGLYCININ, ETC.).
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CC -----
DR EMBL: X06733; CAA29910.1; -

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